



SEQUENCE LISTING

<110> Board of Regents of the University of Texas System

<120> Mutations in a Novel Photoreceptor-pineal gene 17P cause
leber congenital amaurosis (LCA4)

<130> 96606/16UTL

<140> 09/765,061

<141> 2001-01-17

<160> 78

<170> PatentIn version 3.1

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<211> 6689

<212> DNA

<213> Homo sapiens

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<221> gene

<222> (1)..(6689)

<223> the AIPL1 gene produces aryl-hydrocarbon receptor
interacting protein-like 1

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<221> misc_feature

<222> (1897)..(1906)

<223> n represents any of the four nucleotides A T G or C

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interacting protein-like 1

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interacting protein-like 1

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interacting protein-like 1

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aggttgggtg	ggagctgcgg	gttgaaccct	ggggcgaggg	ctggggctat	ggact	1075

<210> 7

<211> 1179

<212> DNA

<213> Macaca mulatta

<220>

<221> gene

<222> (1)..(1179)

<223> the AIPL1 gene produces aryl-hydrocarbon receptor interacting protein-like 1

<400> 7

atggatgccg	ctctgctcct	gaacgtggaa	ggggtaaga	aaaccattct	gcacggaggc	60
acgggagagc	tcccaaactt	catcaccgga	tcccagtgga	tctttcattt	ccgcaccatg	120
aaatgtgatg	aggagcgcac	ggatcatcgac	gacagccgtc	aggtggacca	gcccattgcac	180
atcatcatcg	ggaacatgtt	caagctcgag	gtctgggaga	tcttctcac	ctccatgagg	240
gtgcacgagg	tggccgagtt	ctgggtgcac	accatccaca	cggggggtcta	ccccatctctg	300
tcccggagcc	tgcggcagat	ggcccagggc	aaggaccca	cggagtggca	cgtgcacaca	360
tgcgggctgg	ccaacatgtt	cgcctaccac	acgtgggct	acgaggacct	ggacgagctg	420
cagaaggagc	ctcagcctct	gatctttgtg	atcgagctgc	tgcaggttga	cgccccgagt	480
gattaccaga	gggagacctg	gaacctgagc	aatcatgaga	agatgaaggt	ggtgcccgtc	540
ctccacggag	agggaaatcg	gctcttcaag	ytgggccgct	acgaggaggc	ctcttccaag	600
taccaggagg	ccatcatctg	cctaaggaac	ctgcagacca	aggagaagcc	gtgggaggtg	660
cagtggctga	agctggagaa	gatgatcaac	accctgaccc	tcaactactg	ccagtgcctg	720

ctgaagaagg	aggagtatta	cgaggtgctg	gagcacacca	gtgacattct	ccggcaccac	780
ccaggcatcg	tgaaggccta	ctatgtgctg	gcccgggctc	acgcggaggt	gtggaacgag	840
gccgaggcca	aggcggacct	ccagaaagtg	ctggagctgg	agccatccat	gcagaaggcg	900
gtgcgagggg	agctgaggct	gctggagaac	cgcatggcgg	agaagcagga	ggaggagagg	960
ctgcgctgcc	ggaacatgct	gagccagggg	gccacgcagc	ctcccgaga	gccaccggca	1020
cagcccccca	cagcaccacc	tgcagagctg	tccacagggc	cacctgcgga	cccaccggcg	1080
gagcccccca	cagcaccacc	tgcggagctg	tccacagggc	cacctgcaga	gccaccgcga	1140
gagctcccc	tgtccccagg	gcactcactg	cagcactga			1179

<210> 8

<211> 1119

<212> DNA

<213> Saimiri sciureus

<220>

<221> gene

<222> (1)..(1119)

<223> the AIPL1 gene produces aryl-hydrocarbon receptor interacting protein-like 1

<400> 8

atggatgccg	ctctgctcct	gaacgtggaa	ggggtaaga	agaccattct	gcacgggggc	60
acgggagagc	tcccaaattt	catcaccgga	tcccagtgga	tctttcattt	ccgcaccatg	120
aaatgtgatg	aggagcggac	ggtgattgac	gacagcaggg	aggtgggcca	gcccatgcac	180
atcatcatcg	ggaacatggt	caagctggag	gtctgggaga	tcctgctcac	gtccatgcgg	240
gtgcgagagg	tggccgagtt	ctggtgcgac	accatccaca	cgggggtcta	ccccatcctg	300
tcccggagcc	tgcggcagat	ggcccagggc	aaggaccgga	cggagtggca	tgtgcacacg	360
tgcgggctgg	ccaacatggt	cgctaccac	acgtgggct	acgaggacct	ggatgagctg	420
cagaaggagc	ctcagcctct	gatctttgtg	atcgagctgc	tgcaggttga	tgccccaaagt	480
gattaccaga	gggagacctg	gaacctgagc	aatcacgaga	agatgaaggt	ggtgcccgtc	540
ctccatggag	aaggaaatag	gctcttcaag	ctgggccgct	acgaggaggc	ctcttccaag	600
taccaggagg	ccatcatctg	cctaaggaac	ctgcagacca	aggagaaacc	ctgggaggtg	660
cagtggctga	agctggagaa	gatgatcaat	accctgatcc	tcaactactg	tcagtgtctg	720
ctgaagaagg	aggagtacta	cgaggtcctg	gagcatacca	gtgacattct	ccggcaccac	780
ccaggcattg	tgaaggccta	ctatgtgcgc	gcccgggctc	acgcggaggt	gtggaacgag	840
gccgaggcca	aggcggacct	ccagaaagtg	ctggagctgg	agccgtccat	gcagaaggcg	900
gtgcgagggg	agctgaggct	gctggagaac	cgcatggcgg	agaagcagga	ggaggagcgg	960

ctgcgctgcc gcaacatgct gagccagggg gccacgtggt cccccgcgga gccacccgca 1020
gagccacctg cagagtcata cacagagcca cccgcagagc cacctgcaga gccacctgca 1080
gagctaacct tgaccccgga gcaccacta cagcactga 1119

<210> 9
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon position 79: Met to Thr mutation

<400> 9
acctccacgc ggggtg 15

<210> 10
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> Mutation
<222> (7)..(9)
<223> Amino Acid condon 88 mutation: Trp to X

<400> 10
gagttctgat gcgac 15

<210> 11
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> Mutation
<222> (7)..(9)
<223> Amino Acid condon Mutation position 96: Val to Ile

<400> 11
acggggatct acccc 15

<210> 12
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon mutation position 124: Thr to Ile

<400> 12
gaccccatag agtgg 15

<210> 13
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> Mutation
<222> (7)..(9)
<223> Amino Acid codon mutation position 376: Pro to Ser

<400> 13
ccaccctcgt cccca

15

<210> 14
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon mutation position 163: Gln to X

<400> 14
gattactaga gggag

15

<210> 15
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon mutation position 197: Ala to Pro

<400> 15
gaggagccct cttcc

15

<210> 16
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon mutation: TRP 278 X

<400> 16
gaggtgtgaa atgag

15

<210> 17
<211> 15
<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(7)

<223> a to g mutation: IVS2-2A to G

<400> 17

tccccacggc acacg

15

<210> 18

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Glu 262 Ser

<400> 18

cacccaagtg cgcgg

15

<210> 19

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Arg 302 Leu

<400> 19

gcggtgctca gggag

15

<210> 20

<211> 13

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (5)..(5)

<223> deletion of "TGCAGAGCCACC" sequence

<400> 20

gccaccaca gca

13

<210> 21

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Cys 239 Arg

<400> 21

tgccagcgcc tgctg

15

<210> 22

<211> 13

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (5)..(5)

<223> two base deletion: "AG"

<400> 22

tcccgcagcc acc

13

<210> 23

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Cys 42 X

<400> 23

atgaaatgag atgag

15

<210> 24

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(7)

<223> nine base deletion: "CTCCGGCAC"

<400> 24

gatattcacc ca

12

<210> 25

<211> 21

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(7)

<223> eight base insertion: "GTGATCTT"

<400> 25

gactaggtga tcttgtgatc t

21

<210> 26
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> g to a polymorphism: IVS1-9G to A Benign

<400> 26
ctcagtgact ag

12

<210> 27
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> g to c polymorphism: IVS2+66G to C Benign

<400> 27
tttgccgggc tg

12

<210> 28
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> c to t polymorphism: IVS2-88C to T Benign

<400> 28
tcctctcagg ag

12

<210> 29
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> g to a polymorphism: IVS2-14G to A Benign

<400> 29
atccatttat cc

12

<210> 30
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> a to c mutation: IVS2-10A to C Benign

<400> 30
cgtttctccc ca

12

<210> 31
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> t to c mutation: IVS3-25T to C Benign

<400> 31
ctgccccact ga

12

<210> 32
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(7)
<223> t to c mutation: IVS3-21T to C Benign

<400> 32
cctcaccgac ct

12

<210> 33
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(7)
<223> g to a mutation: IVS5+18G to A Benign

<400> 33
aggagcggac ag

12

<210> 34
<211> 12
<212> DNA
<213> Homo sapiens

<220>

<221> mutation
<222> (7)..(9)
<223> Amino Acid codon mutation: Asp 90 His Benign

<400> 34
tggtgccaca cc

12

<210> 35
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid mutation: Phe 37 Phe Benign

<400> 35
catttccgca cc

12

<210> 36
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid mutation: Ser 78 Ser Benign

<400> 36
acctctatgc gg

12

<210> 37
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid mutation: Cys 89 Cys Benign

<400> 37
tggtgtgaca cc

12

<210> 38
<211> 12
<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid codon mutation: Leu 100 Leu Benign

<400> 38

atcctgtccc gg

12

<210> 39

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid codon mutation: His 172 His

<400> 39

aatcacgaga ag

12

<210> 40

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid codon mutation: Pro 217 Pro Benign

<400> 40

aagccgtggg ag

12

<210> 41

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid codon mutation: Asp 255 Asp Benign

<400> 41

agtgacattc tc

12

<210> 42
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)..(20)
<223> 5' to 3' primer sequence

<400> 42
aagaaaacca ttctgcacgg

20

<210> 43
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)..(19)
<223> 5' to 3' primer sequence

<400> 43
tgcagctcgt ccaggtcct

19

<210> 44
<211> 17
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)..(17)
<223> 5' to 3' primer sequence

<400> 44
gacacctccc tttctcc

17

<210> 45
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)..(18)
<223> 5' to 3' primer sequence

<400> 45
gctggggctg cctggctg

18

<210> 46
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)..(20)
<223> 5' to 3' primer sequence

<400> 46
ccgagtgatt accagagggga. 20

<210> 47
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)..(20)
<223> 5' to 3' primer sequence

<400> 47
tgagctccag cacctcatag. 20

<210> 48
<211> 18
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(18)
<223> 5' to 3' primer sequence

<400> 48
acgcagaggt gtggaatg 18

<210> 49
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)..(19)
<223> 5' to 3' primer sequence

19

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<220>
<221> misc_binding
<222> (1)..(34)
<223> exon/intron - donor splice site:
CGGATCCCCGAgtagtggggccctccggagca
      ga
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34

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<220>
<221> misc_binding
<222> (1)..(35)
<223> exon/intron Acceptor splice site:
cagagtgccacggtctcggtgactagGTGATC
      TTTC
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35

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<220>
<221> misc_binding
<222> (1)..(35)
<223> exon/intron Donor splice site:
CSACACCATCgtaagtaggcctgcgcgcctgtc
t
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35

<210> 53

<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> misc_binding
<222> (1)..(35)
<223> exon/intron Acceptor splice site:
gccatccatccgtttatccccacagCACACG
GGGG

<400> 53
gccatccatc cgtttatccc cacagcacac ggggg

35

<210> 54
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> misc_binding
<222> (1)..(35)
<223> exon/intron Donor splice site:
GCTGCTGCAGgtggggctgggggtggcagggct
; gg

<400> 54
gctgctgcag gtggggctgg ggttggcagg gctgg

35

<210> 55
<211> 35
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(35)
<223> exon/intron Acceptor splice site:
cactgacctgcagctctggggccagGTTGA
TGCCC

<400> 55
cactgacctg cagctctggg gccaggttga tgccc

35

<210> 56
<211> 35
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(35)

<223> exon/intron Donor splice site:
GCAGACCAAGgtcagaggccgctggccacggggt
g

<400> 56
gcagaccaag gtcagaggcc gctggccacg ggggtg

35

<210> 57
<211> 35
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(35)
<223> exon/intron Acceptor splice site:
catggctgaccttctccctgggcagGAGAA
GCCRT

<400> 57
catggctgac cttctccctg ggcaggagaa gccrt

35

<210> 58
<211> 35
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(35)
<223> exon/intron Donor splice site:
CACCACCCAGgtgcgcggggctgcaggggcgga
ca

<400> 58
caccaccag gtgcgcgggg ctgcaggggc ggaca

35

<210> 59
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> misc_binding
<222> (1)..(35)
<223> exon/intron Acceptor splice site:
gctggatgctccctgctccccacagGCATC
GTGAA

<400> 59
gctggatgct ccctgctccc cacaggcatc gtgaa

35

<210> 60
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(18)
<223> AIPL1 gene exon 1 Primer 5' to 3'

<400> 60
gga cac ctc cct ttc tcc
Gly His Leu Pro Phe Ser
1 5 18

<210> 61
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(18)
<223> AIPL1 gene exon 1 Primer 5' to 3'

<400> 61
gct ggg gct gcc tgg ctg
Ala Gly Ala Ala Trp Leu
1 5 18

<210> 62
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(20)
<223> AIPL1 gene exon 2 Primer 5' to 3'

<400> 62
ggg cct tga aca gtg tgt ct
Gly Pro Thr Val Cys
1 5 20

<210> 63
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(19)
<223> AIPL1 gene exon 2 Primer 5' to 3'

<400> 63
ttt ccc gaa aca cag cag c
Phe Pro Glu Thr Gln Gln
1 5

19

<210> 64
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(18)
<223> AIPL1 gene exon 3 Primer 5' to 3'

<400> 64
agt gag gga gca gga ttc
Ser Glu Gly Ala Gly Phe
1 5

18

<210> 65
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(20)
<223> AIPL1 gene exon 3 Primer 5' to 3'

<400> 65
tgc cca tga tgc ccg ctg tc
Cys Pro Cys Pro Leu
1 5

20

<210> 66
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(18)
<223> AIPL1 gene exon 4 Primer 5' to 3'

<400> 66
ttt cgg gtc tct gat ggg
Phe Arg Val Ser Asp Gly
1 5

18

<210> 67
<211> 17
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(17)
<223> AIPL1 gene exon 4 Primer 5' to 3'

<400> 67
gca ggc tcc cca gag tc
Ala Gly Ser Pro Glu
1 5

17

<210> 68
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(19)
<223> AIPL1 gene exon 5 Primer 5' to 3'

<400> 68
gca gct gcc tca ggt cat g
Ala Ala Ala Ser Gly His
1 5

19

<210> 69
<211> 18
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(18)

<223> AIPL1 gene exon 5 Primer 5' to 3'

<400> 69

gtg ggg tgg aaa gaa aag
Val Gly Trp Lys Glu Lys
1 5

18

<210> 70

<211> 18

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(18)

<223> AIPL1 gene exon 6 Primer 5' to 3'

<400> 70

ctg gga agg gag ctg tag
Leu Gly Arg Glu Leu
1 5

18

<210> 71

<211> 19

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(19)

<223> AIPL1 gene exon 6 Primer 5' to 3'

<400> 71

aaa agt gac acc acg atc c
Lys Ser Asp Thr Thr Ile
1 5

19

<210> 72

<211> 384

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(384)

<223> Human AIPL1 Protein

<220>

<221> misc_feature

<222> (322)..(322)

<223> Xaa represents any of the twenty amino acids

<400> 72

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr	
1				5					10					15	
Ile	Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly	
				20					25					30	
Ser	Arg	Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	
				35					40					45	
Arg	Thr	Val	Ile	Asp	Asp	Ser	Arg	Gln	Val	Gly	Gln	Pro	Met	His	
				50					55					60	
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	
				65					70					75	
Leu	Thr	Ser	Met	Arg	Val	His	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	
				80					85					90	
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg	
				95					100					105	
Gln	Met	Ala	Gln	Gly	Lys	Asp	Pro	Thr	Glu	Trp	His	Val	His	Thr	
				110					115					120	
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu	
				125					130					135	
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Val	Phe	Val	
				140					145					150	
Ile	Glu	Leu	Leu	Gln	Val	Asp	Ala	Pro	Ser	Asp	Tyr	Gln	Arg	Glu	
				155					160					165	
Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys	Ala	Val	Pro	Val	
				170					175					180	
Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	Arg	Tyr	Glu	
				185					190					195	
Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu	Arg	Asn	
				200					205					210	
Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	Leu	
				215					220					225	
Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu	
				230					235					240	
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp	
				245					250					255	
Ile	Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg	
				260					265					270	
Ala	Arg	Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala	

	275		280		285
Asp Leu Gln Lys	Val Leu Glu Leu Glu	Pro Ser Met Gln Lys	Ala		
	290		295		300
Val Arg Arg Glu	Leu Arg Leu Leu Glu	Asn Arg Met Ala Glu	Lys		
	305		310		315
Gln Glu Glu Glu	Arg Leu Xaa Cys Arg	Asn Met Leu Ser Gln	Gly		
	320		325		330
Ala Thr Gln Pro	Pro Ala Glu Pro Pro	Thr Glu Pro Pro Ala	Gln		
	335		340		345
Ser Ser Thr Glu	Pro Pro Ala Glu Pro	Pro Thr Ala Pro Ser	Ala		
	350		355		360
Glu Leu Ser Ala	Gly Pro Pro Ala Glu	Pro Ala Thr Glu Pro	Pro		
	365		370		375
Pro Ser Pro Gly	His Ser Leu Gln His				
	380				

<210> 73
 <211> 384
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> PEPTIDE
 <222> (1)..(384)
 <223> Chimpanzee AIPL1 Protein

<400> 73

Met Asp Ala Ala	Leu Leu Leu Asn Val	Glu Gly Val Lys Lys Thr Ile
1	5	10 15
Leu His Gly Gly	Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg	
	20	25 30
Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val		
	35	40 45
Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly		
	50	55 60
Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg		
	65	70 75 80
Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val		
	85	90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Ala Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Arg
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Thr Glu Pro Pro Ala Gln Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Pro Ala Pro Ser Ala Glu Leu Ser Ala Gly Pro Pro Ala
355 360 365

Glu Thr Ala Thr Glu Pro Pro Pro Ser Pro Gly His Ser Leu Gln His
370 375 380

<210> 74
<211> 372
<212> PRT
<213> Papio anubis

<220>
<221> PEPTIDE
<222> (1)..(372)
<223> Baboon AIPL1 Protein

<400> 74

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Thr
325 330 335

Glu Pro Pro Ala Glu Pro His Thr Ala Pro Pro Ala Glu Leu Ser Thr
340 345 350

Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu Ser Pro Gly His
355 360 365

Ser Leu Gln His
370

<210> 75
<211> 328
<212> PRT
<213> Bos taurus

<220>
<221> PEPTIDE
<222> (1)..(328)
<223> Cow AIPL1 Protein

<400> 75

Met Asp Ala Thr Leu Leu Leu Asn Val Glu Gly Ile Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Asp Leu Pro Asn Phe Ile Thr Gly Ala Arg
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly His Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val Ser Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Glu Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Ile Ile Glu Leu Leu Gln Val Glu Ala Pro Ser
145 150 155 160

Gln Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Gln Glu Lys Met Gln
165 170 175

Ala Val Pro Ile Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Asn Lys Tyr Gln Glu Ala Ile Val Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Glu
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Gln Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Leu Glu Glu Lys Arg Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Gly
325

<210> 76
<211> 328
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(328)
<223> Mouse AIPL1 Protein

<400> 76

Met Asp Val Ser Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly Gln Pro Met Ser Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Thr Leu Leu Thr Ser Met Arg
65 70 75 80

Leu Gly Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Met Leu Ser Arg Ser Leu Arg Gln Val Ala Glu Gly Lys Asp
100 105 110

Pro Thr Ser Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Val Phe Leu Tyr Glu Leu Leu Gln Val Glu Ala Pro Asn
145 150 155 160

Glu Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Glu Glu Arg Met Gln
165 170 175

Ala Val Pro Leu Leu His Gly Glu Gly Asn Arg Leu Tyr Lys Leu Gly
180 185 190

Arg Tyr Asp Gln Ala Ala Thr Lys Tyr Gln Glu Ala Ile Val Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Glu Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Met Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly
325

<210> 77
<211> 392
<212> PRT
<213> Macaca mulatta

<220>
<221> PEPTIDE
<222> (1)..(392)
<223> Rhesus Monkey AIPL1 Protein

<400> 77

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Ala Gln Pro Pro Thr Ala Pro Pro Ala Glu Leu Ser Thr
340 345 350

Gly Pro Pro Ala Asp Pro Pro Ala Glu Pro Pro Thr Ala Pro Pro Ala
355 360 365

Glu Leu Ser Thr Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu
370 375 380

Ser Pro Gly His Ser Leu Gln His
385 390

<210> 78
<211> 372
<212> PRT
<213> Saimiri sciureus

<220>
<221> PEPTIDE
<222> (1)..(372)
<223> Squirrel Monkey AIPL1 Protein

<400> 78

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Glu Val Gly Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val Arg Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Trp Ser Pro Ala
325 330 335

Glu Pro Pro Ala Glu Pro Pro Ala Glu Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Ala Glu Pro Pro Ala Glu Leu Thr Leu Thr Pro Gly His
355 360 365

Pro Leu Gln His
370

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